

# Sequence Listing

<110> KANEKA CORPORATION

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE PYRIDINEETHANOL DERIVATIVES

<130> KN312W0

<150> JP P1999-206503

<151> 1999-07-21

<160> 2

<210> 1

<211> 254

<212> PRT

<213> *Candida maris*

<400> 1

Met Ser Tyr Asn Phe Ala Asn Lys Val Leu Ile Val Thr Gly Gly Leu  
1 5 10 15  
Ser Gly Ile Gly Leu Ala Val Ala Lys Lys Phe Leu Gln Leu Gly Ala  
20 25 30  
Lys Val Thr Ile Ser Asp Ile Ser Ala Thr Glu Lys Tyr Asn Thr Val  
35 40 45  
Val Gly Glu Phe Lys Thr Glu Gly Ile Asp Val Lys Asn Val Gln Tyr  
50 55 60  
Ile Gln Ala Asp Ala Ser Lys Glu Ala Asp Asn Glu Lys Leu Ile Ser  
65 70 75 80  
Glu Thr Leu Ser Ala Phe Gly Asp Leu Asp Tyr Val Cys Ala Asn Ala  
85 90 95  
Gly Ile Ala Thr Phe Thr Gln Thr Thr Asp Ile Ser Tyr Asp Val Trp  
100 105 110  
Arg Lys Val Thr Ser Ile Asn Leu Asp Gly Val Phe Met Leu Asp Lys  
115 120 125  
Leu Ala Ala Gln Tyr Phe Leu Ser Lys Asn Lys Pro Gly Ala Ile Val  
130 135 140  
Asn Met Gly Ser Ile His Ser Tyr Val Ala Ala Pro Gly Leu Ser His  
145 150 155 160  
Tyr Gly Ala Ala Lys Gly Gly Leu Lys Leu Leu Thr Gln Thr Met Ala  
165 170 175  
Leu Glu Tyr Ala Ala Lys Gly Ile Arg Val Asn Ser Val Asn Pro Gly

	180		185		190										
Tyr	Ile	Lys	Thr	Pro	Leu	Leu	Asp	Ile	Cys	Pro	Lys	Glu	His	Met	Asp
	195				200				205						
Tyr	Leu	Ile	Thr	Gln	His	Pro	Ile	Gly	Arg	Leu	Gly	Lys	Pro	Glu	Glu
	210				215				220						
Ile	Ala	Ser	Ala	Val	Ala	Phe	Leu	Cys	Ser	Asp	Glu	Ala	Thr	Phe	Ile
225				230					235					240	
Asn	Gly	Ile	Ser	Leu	Leu	Val	Asp	Gly	Gly	Tyr	Thr	Ala	Arg		
			245					250							

<210> 2

<211> 765

<212> DNA

<213> Candida maris

<400> 2

atg	tcc	tac	aat	ttt	gcc	aac	aaa	gtt	ctt	att	gtg	acc	gga	ggt	ctg
Met	Ser	Tyr	Asn	Phe	Ala	Asn	Lys	Val	Leu	Ile	Val	Thr	Gly	Gly	Leu
1			5					10					15		
tcc	ggt	att	gga	ctt	gca	gtt	gca	aag	aag	ttt	ctt	caa	ctc	ggg	gcc
Ser	Gly	Ile	Gly	Leu	Ala	Val	Ala	Lys	Lys	Phe	Leu	Gln	Leu	Gly	Ala
			20					25					30		
aaa	gtg	aca	att	tct	gat	att	tct	gcc	act	gaa	aag	tac	aac	acg	gtt
Lys	Val	Thr	Ile	Ser	Asp	Ile	Ser	Ala	Thr	Glu	Lys	Tyr	Asn	Thr	Val
			35					40					45		
gta	ggt	gag	ttc	aaa	acc	gag	ggc	att	gat	gtc	aag	aat	gtt	cag	tat
Val	Gly	Glu	Phe	Lys	Thr	Glu	Gly	Ile	Asp	Val	Lys	Asn	Val	Gln	Tyr
	50					55					60				
att	cag	gcc	gat	gca	agc	aaa	gag	gcc	gac	aac	gag	aag	ctc	atc	tcc
Ile	Gln	Ala	Asp	Ala	Ser	Lys	Glu	Ala	Asp	Asn	Glu	Lys	Leu	Ile	Ser
65				70					75					80	
gag	aca	ctg	tct	gct	ttc	ggt	gat	ctc	gac	tac	gtg	tgc	gca	aat	gct
Glu	Thr	Leu	Ser	Ala	Phe	Gly	Asp	Leu	Asp	Tyr	Val	Cys	Ala	Asn	Ala
				85					90					95	
gga	att	gcc	act	ttc	aca	cag	act	aca	gat	atc	tcc	tac	gac	gtc	tgg
Gly	Ile	Ala	Thr	Phe	Thr	Gln	Thr	Thr	Asp	Ile	Ser	Tyr	Asp	Val	Trp
				100					105					110	

agg aag gta acc agc att aat ctt gac ggt gtt ttc atg ctt gat aaa  
 Arg Lys Val Thr Ser Ile Asn Leu Asp Gly Val Phe Met Leu Asp Lys  
 115 120 125  
 cta gct gca caa tac ttt ttg agc aag aac aag cca ggt gct att gtc  
 Leu Ala Ala Gln Tyr Phe Leu Ser Lys Asn Lys Pro Gly Ala Ile Val  
 130 135 140  
 aac atg ggt tcc att cac tcg tat gtg gcc gct cct gga ctt tct cac  
 Asn Met Gly Ser Ile His Ser Tyr Val Ala Ala Pro Gly Leu Ser His  
 145 150 155 160  
 tac ggt gcg gcc aaa gga ggt ctg aag cta ctg act cag acc atg gcc  
 Tyr Gly Ala Ala Lys Gly Gly Leu Lys Leu Leu Thr Gln Thr Met Ala  
 165 170 175  
 ctt gag tat gcc gca aaa ggt ata aga gtt aac tcg gtc aat cct ggt  
 Leu Glu Tyr Ala Ala Lys Gly Ile Arg Val Asn Ser Val Asn Pro Gly  
 180 185 190  
 tac atc aag aca cca ttg ctt gat att tgc cct aaa gaa cac atg gat  
 Tyr Ile Lys Thr Pro Leu Leu Asp Ile Cys Pro Lys Glu His Met Asp  
 195 200 205  
 tac ctt atc act cag cat cca att gga cgt ctc gga aag cct gaa gag  
 Tyr Leu Ile Thr Gln His Pro Ile Gly Arg Leu Gly Lys Pro Glu Glu  
 210 215 220  
 att gca agt gct gtt gca ttt ctg tgc tct gac gag gct aca ttt atc  
 Ile Ala Ser Ala Val Ala Phe Leu Cys Ser Asp Glu Ala Thr Phe Ile  
 225 230 235 240  
 aac gga atc tcc ttg ttg gta gac ggt ggt tat acc gca aga taa  
 Asn Gly Ile Ser Leu Leu Val Asp Gly Gly Tyr Thr Ala Arg  
 245 250